

04CO  
04-28-01. 0420 #3

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/803,589

DATE: 03/30/2001

TIME: 12:29:59

Input Set : A:\07334-325001.TXT

Output Set: N:\CRF3\03302001\I803589.raw

4 <110> APPLICANT: McCarthy, Sean A.  
5 Holtzman, Douglas A.  
6 Goodearl, Andrew D.J.  
8 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
9 PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER  
10 USES  
12 <130> FILE REFERENCE: 07334-325001  
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/803,589  
C--> 14 <141> CURRENT FILING DATE: 2001-03-09  
14 <150> PRIOR APPLICATION NUMBER: US 09/128,709  
15 <151> PRIOR FILING DATE: 1998-08-04  
17 <150> PRIOR APPLICATION NUMBER: US 60/054,645  
18 <151> PRIOR FILING DATE: 1997-08-04  
20 <150> PRIOR APPLICATION NUMBER: US 09/130,491  
21 <151> PRIOR FILING DATE: 1998-08-06  
23 <150> PRIOR APPLICATION NUMBER: US 60/054,966  
24 <151> PRIOR FILING DATE: 1997-08-06  
26 <150> PRIOR APPLICATION NUMBER: US 60/058,108  
27 <151> PRIOR FILING DATE: 1997-09-05  
29 <150> PRIOR APPLICATION NUMBER: US 09/388,280  
30 <151> PRIOR FILING DATE: 1999-09-01  
32 <150> PRIOR APPLICATION NUMBER: US 09/388,279  
33 <151> PRIOR FILING DATE: 1999-09-01  
35 <160> NUMBER OF SEQ ID NOS: 14  
37 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
39 <210> SEQ ID NO: 1  
40 <211> LENGTH: 3147  
41 <212> TYPE: DNA  
42 <213> ORGANISM: Homo sapiens  
44 <220> FEATURE:  
45 <221> NAME/KEY: CDS  
46 <222> LOCATION: (3)...(1826)  
48 <400> SEQUENCE: 1  
49 cc acg cgt ccg atc ttg gtc atc cac gat gaa cag aag ggg ccg gaa 47  
50 Thr Arg Pro Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu  
51 1 5 10 15  
53 gtg acc tcc aat gct gcc ctc act ctg cgg aac ttt tgc aac tgg cag 95  
54 Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln  
55 20 25 30  
57 aag cag cac aac cca ccc agt gac cgg gat gca gag cac tat gac aca 143  
58 Lys Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr  
59 35 40 45  
61 gca att ctt ttc acc aga cag gac ttg tgt ggg tcc cag aca tgt gat 191  
62 Ala Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp  
63 50 55 60  
65 act ctt ggg atg gct gat gtt gga act gtg tgt gat ccg agc aga agc 239  
66 Thr Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser

ENTERED

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67      65      70      75
69 tgc tcc gtc ata gaa gat gat ggt tta caa gct gcc ttc acc aca gcc      287
70 Cys Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala
71 80      85      90      95
73 cat gaa tta ggc cac gtg ttt aac atg cca cat gat gat gca aag cag      335
74 His Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln
75      100      105      110
77 tgt gcc agc ctt aat ggt gtg aac cag gat tcc cac atg atg gcg tca      383
78 Cys Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser
79      115      120      125
81 atg ctt tcc aac ctg gac cac agc cag cct tgg tct cct tgc agt gcc      431
82 Met Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala
83      130      135      140
85 tac atg att aca tca ttt ctg gat aat ggt cat ggg gaa tgt ttg atg      479
86 Tyr Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met
87      145      150      155
89 gac aag cct cag aat ccc ata cag ctc cca ggc gat ctc cct ggc acc      527
90 Asp Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr
91 160      165      170      175
93 tcg tac gat gcc aac cgg cag tgc cag ttt aca ttt ggg gag gac tcc      575
94 Ser Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp Ser
95      180      185      190
97 aaa cac tgc ccc gat gca gcc agc aca tgt agc acc ttg tgg tgt acc      623
98 Lys His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr
99      195      200      205
101 ggc acc tct ggt ggg gtg ctg gtg tgt caa acc aaa cac ttc ccg tgg      671
102 Gly Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp
103      210      215      220
105 gcg gat ggc acc agc tgt gga gaa ggg aaa tgg tgt atc aac ggc aag      719
106 Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys
107      225      230      235
109 tgt gtg aac aaa acc gac aga aag cat ttt gat acg cct ttt cat gga      767
110 Cys Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His Gly
111 240      245      250      255
113 agc tgg gga atg tgg ggg cct tgg gga gac tgt tcg aga acg tgc ggt      815
114 Ser Trp Gly Met Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly
115      260      265      270
117 gga gga gtc cag tac acg atg agg gaa tgt gac aac cca gtc cca aag      863
118 Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro Lys
119      275      280      285
121 aat gga ggg aag tac tgt gaa ggc aaa cga gtg cgc tac aga tcc tgt      911
122 Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys
123      290      295      300
125 aac ctt gag gac tgt cca gac aat aat gga aaa acc ttt aga gag gaa      959
126 Asn Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu
127      305      310      315
129 caa tgt gaa gca cac aac gag ttt tca aaa gct tcc ttt ggg agt ggg      1007
130 Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly
131 320      325      330      335
```

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```
133 cct gcg gtg gaa tgg att ccc aag tac gct ggc gtc tca cca aag gac 1055
134 Pro Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp
135 340 345 350
137 agg tgc aag ctc atc tgc caa gcc aaa ggc att ggc tac ttc ttc gtt 1103
138 Arg Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val
139 355 360 365
141 ttg cag ccc aag gtt gta gat ggt act cca tgt agc cca gat tcc acc 1151
142 Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr
143 370 375 380
145 tct gtc tgt gtg caa gga cag tgt gta aaa gct ggt tgt gat cgc atc 1199
146 Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile
147 385 390 395
149 ata gac tcc aaa aag aag ttt gat aaa tgt ggt gtt tgc ggc gga aat 1247
150 Ile Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn
151 400 405 410 415
153 gga tct act tgt aaa aaa ata tca gga tca gtt act agt gca aaa cct 1295
154 Gly Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro
155 420 425 430
157 gga tat cat gat atc atc aca att cca act gga gcc acc aac atc gaa 1343
158 Gly Tyr His Asp Ile Ile Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu
159 435 440 445
161 gtg aaa cag cgg aac cag agg gga tcc agg aac aat ggc agc ttt ctt 1391
162 Val Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu
163 450 455 460
165 gcc atc aaa gct gct gat ggc aca tat att ctt aat ggt gac tac act 1439
166 Ala Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr
167 465 470 475
169 ttg tcc acc tta gag caa gac att atg tac aaa ggt gtt gtc ttg agg 1487
170 Leu Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg
171 480 485 490 495
173 tac agc ggc tcc tct gcg gca ttg gaa aga att cgc agc ttt agc cct 1535
174 Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro
175 500 505 510
177 ctc aaa gag ccc ttg acc atc cag gtt ctt act gtg ggc aat gcc ctt 1583
178 Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu
179 515 520 525
181 cga cct aaa att aaa tac acc tac ttc gta aag aag aag aag gaa tct 1631
182 Arg Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser
183 530 535 540
185 ttc aat gct atc ccc act ttt tca gca tgg gtc att gaa gag tgg ggc 1679
186 Phe Asn Ala Ile Pro Thr Phe Ser Ala Trp Val Ile Glu Glu Trp Gly
187 545 550 555
189 gaa tgt tct aag acc tgt ggg aag ggt tac aaa aaa aga agc ttg aag 1727
190 Glu Cys Ser Lys Thr Cys Gly Lys Gly Tyr Lys Lys Arg Ser Leu Lys
191 560 565 570 575
193 tgt ctg tcc cat gat gga ggg gtg tta tct cat gag agc tgt gat cct 1775
194 Cys Leu Ser His Asp Gly Gly Val Leu Ser His Glu Ser Cys Asp Pro
195 580 585 590
197 tta aag aaa cct aaa cat ttc ata gac ttt tgc aca atg gca gaa tgc 1823
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```

198 Leu Lys Lys Pro Lys His Phe Ile Asp Phe Cys Thr Met Ala Glu Cys
199          595          600          605
201 agt taagtgggttt aagtgggtgtt agcttttgagg gcaaggcaaa gtgaggaagg      1876
202 Ser
204 gctgggtgcag ggaaagcaag aaggctggag ggatccagcg tatcttgcca gtaaccagtg      1936
205 aggtgtatca gtaaggtggg attatggggg tagatagaaa aggagttgaa tcatcagagt      1996
206 aaactgccag ttgcaaatTT gataggatag ttagtggaga ttattaacct ctgagcagtg      2056
207 atatagcata ataaagcccc gggcattatt attattattt cttttgttac atctattaca      2116
208 agtttagaaa aaacaaagca attgtcaaaa aaagttagaa ctattacaac cctgtttcc      2176
209 tgggtacttat caaatactta gtatcatggg ggttgggaaa tgaaaagtag gagaaaagtg      2236
210 agattttact aagacctgtt ttactttacc tcactaacia tggggggaga aaggagtaca      2296
211 aataggatct ttgaccagca ctgtttatgg ctgctgtggt ttcagagaat gtttatacat      2356
212 tattttctacc gagaattaaa acttcagatt gttcaacatg agagaaaggc tcagcaacgt      2416
213 gaaataacgc aaatggcttc ctctttcctt ttttggacca tctcagtcct tatttgtgta      2476
214 attcattttg aggaaaaaac aactccatgt atttattcaa gtgcattaaa gtctacaatg      2536
215 gaaaaaaaagc agtgaagcat tacatgctgg taaaagctag aggagacaca atgagcttag      2596
216 tacctcaaac ttcttttctt tcttaccatg taacctgctt ttcggaatat ggatgtaaag      2656
217 aagtaacttg tgtctcatga aaatcagtac aatcacacia ggaggatgaa acgcccgaac      2716
218 aaaaatgagg tgtgtagaac aggtgcccac aggtttgggg acattgagat cacttgtctt      2776
219 gtgggtgggga ggtgctgtag gggtagcagg tccatctcca gcagctgggc caacagtcgt      2836
220 atcctggtga atgtctgttc agctcttctg tgagaatatg attttttcca tatgtatata      2896
221 gtaaaatatg ttactataaa ttacatgtac tttataagta ttggtttggg tgttcttcc      2956
222 aagaaggact atagttagta ataaatgcct ataataacat atttattttt atacatttat      3016
223 ttctaataga aaaaactttt aaattatatc gcttttgtgg aagtgcatat aaaatagagt      3076
224 atttatacaa tatatgttac tagaaataaa agaacacttt tggaaaaaaa aaaaaaaaaa      3136
225 agggcgccgc c                                     3147
227 <210> SEQ ID NO: 2
228 <211> LENGTH: 608
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
232 <400> SEQUENCE: 2
233 Thr Arg Pro Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu Val
234 1          5          10          15
235 Thr Ser Asn Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln Lys
236          20          25          30
237 Gln His Asn Pro Pro Ser Asp Arg Asp Ala Glu His Tyr Asp Thr Ala
238          35          40          45
239 Ile Leu Phe Thr Arg Gln Asp Leu Cys Gly Ser Gln Thr Cys Asp Thr
240          50          55          60
241 Leu Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ser Arg Ser Cys
242 65          70          75          80
243 Ser Val Ile Glu Asp Asp Gly Leu Gln Ala Ala Phe Thr Thr Ala His
244          85          90          95
245 Glu Leu Gly His Val Phe Asn Met Pro His Asp Asp Ala Lys Gln Cys
246          100         105         110
247 Ala Ser Leu Asn Gly Val Asn Gln Asp Ser His Met Met Ala Ser Met
248          115         120         125
249 Leu Ser Asn Leu Asp His Ser Gln Pro Trp Ser Pro Cys Ser Ala Tyr
250          130         135         140

```

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```

251 Met Ile Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu Met Asp
252 145 150 155 160
253 Lys Pro Gln Asn Pro Ile Gln Leu Pro Gly Asp Leu Pro Gly Thr Ser
254 165 170 175
255 Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu Asp Ser Lys
256 180 185 190
257 His Cys Pro Asp Ala Ala Ser Thr Cys Ser Thr Leu Trp Cys Thr Gly
258 195 200 205
259 Thr Ser Gly Gly Val Leu Val Cys Gln Thr Lys His Phe Pro Trp Ala
260 210 215 220
261 Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Ile Asn Gly Lys Cys
262 225 230 235 240
263 Val Asn Lys Thr Asp Arg Lys His Phe Asp Thr Pro Phe His Gly Ser
264 245 250 255
265 Trp Gly Met Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly
266 260 265 270
267 Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro Lys Asn
268 275 280 285
269 Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser Cys Asn
270 290 295 300
271 Leu Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu Glu Gln
272 305 310 315 320
273 Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Ser Gly Pro
274 325 330 335
275 Ala Val Glu Trp Ile Pro Lys Tyr Ala Gly Val Ser Pro Lys Asp Arg
276 340 345 350
277 Cys Lys Leu Ile Cys Gln Ala Lys Gly Ile Gly Tyr Phe Phe Val Leu
278 355 360 365
279 Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser Thr Ser
280 370 375 380
281 Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg Ile Ile
282 385 390 395 400
283 Asp Ser Lys Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly Asn Gly
284 405 410 415
285 Ser Thr Cys Lys Lys Ile Ser Gly Ser Val Thr Ser Ala Lys Pro Gly
286 420 425 430
287 Tyr His Asp Ile Ile Thr Ile Pro Thr Gly Ala Thr Asn Ile Glu Val
288 435 440 445
289 Lys Gln Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe Leu Ala
290 450 455 460
291 Ile Lys Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asp Tyr Thr Leu
292 465 470 475 480
293 Ser Thr Leu Glu Gln Asp Ile Met Tyr Lys Gly Val Val Leu Arg Tyr
294 485 490 495
295 Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser Pro Leu
296 500 505 510
297 Lys Glu Pro Leu Thr Ile Gln Val Leu Thr Val Gly Asn Ala Leu Arg
298 515 520 525
299 Pro Lys Ile Lys Tyr Thr Tyr Phe Val Lys Lys Lys Lys Glu Ser Phe

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/803,589

DATE: 03/30/2001

TIME: 12:30:00

Input Set : A:\07334-325001.TXT

Output Set: N:\CRF3\03302001\I803589.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application NO

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date